Developmental and Comparative Immunology 39 (2013) 11–26

Contents lists available at SciVerse ScienceDirect

Developmental and Comparative Immunology

journal homepage: www.elsevier.com/locate/dci

Review

Recent advances in researches on the innate immunity of shrimp in China

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ARTICLE INFO

Article history:
Available online 3 April 2012

Keywords:
Shrimp immunity
Pattern recognition receptor
Signal pathway
Immune homeostasis
WSSV
Mainland of China

ABSTRACT

The annual production of shrimp culture in mainland of China has been over one million tons for several years. The major cultivated penaeidae species are *Litopenaeus vannamei, Fenneropenaeus chinensis*, *Penaeus monodon* and *Marsupenaeus japonicus*. Due to the importance of shrimp aquaculture in China, researchers have paid more attention to the molecular mechanism of shrimp disease occurrence and tried to develop an efficient control strategy for disease. This paper summarizes the research progress related to innate immunity of penaeid shrimp made in the last decade in Mainland China. Several pattern recognition receptors, such as lectin, toll, lipopolysaccharide and β-1,3-glucan binding protein (LGBP) and tetraspanin were identified. The major signal transduction pathways, including Toll pathway, IMD pathway, which might be involved in the immune response of shrimp, were focused on and most of the components in Toll pathway were identified. Also, cellular immune responses such as phagocytosis and apoptosis were regarded playing very important roles in anti-WSSV infection to shrimp. The molecules involved in the maintenance of the immune homeostasis of shrimp and the progress on molecular structure and pathogenic mechanism of WSSV were summarized. Therefore, the brief outline about the immune system of shrimp is drawn based on the recent data which will help us to understand the immune responses of shrimp to different pathogens.

Contents

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0145-305X/$ - see front matter © 2012 Elsevier Ltd. All rights reserved.
http://dx.doi.org/10.1016/j.dci.2012.03.016

1. Introduction

Shrimp products provide a certain amount of animal protein and become very important in people's life. According to statistics of the Food and Agriculture Organization (FAO) of the United Nations, marine and brackish water shrimp culture production in the world expanded from 8987 metric tons in 1970 to 3,146,918 metric tons in 2006. The spectacular increase in cultivated shrimp production has occurred despite relatively poor basic knowledge of the cultivated species and enormous losses due to diseases, estimated at approximately US $1 billion per year since the early 1990s (Flegel et al., 2008). In China, shrimp aquaculture industry initiated in the early 1980s, and the production of shrimp aquaculture increased very quickly and reached 200,000 metric tons in 1992. However, due to the outbreak of white spot syndrome virus (WSSV) disease in shrimp aquaculture in China, its production decreased dramatically to about 50,000 metric tons. Since the introduction and culture of *Litopenaeus vannamei* (*L. vannamei*), the total shrimp production in mainland of China reached 1,024,000 metric tons in 2006 (data from the Agriculture Ministry of China) which accounted for nearly one third of the world's total production. The main shrimp species cultured in China include *L. vannamei*, *Fenneropenaeus chinensis* (*F. chinensis*), *Penaeus monodon* (*P. monodon*), *Marsupenaeus japonicus* (*M. japonicus*), and only the culture production of *L. vannamei* accounts for about 85% of the total shrimp production in mainland of China. Disease is always a problem which harasses the healthy development of shrimp aquaculture. Both virus and bacteria can be dangerous pathogens of shrimp in aquaculture. Application of traditional antibiotics can alleviate bacteria disease, but traditional strategy used to prevent virus disease in vertebrate is not effective to cure virus disease of shrimp since no adaptive immunity exists in them. WSSV is one of the most dangerous pathogen that is highly virulent in penaeid shrimp. WSSV infection of penaeid shrimp can result in mortality of up to 90–100%. Although the great majority of the disease losses was caused by viral pathogens, little work was published on the shrimp response to viral pathogens before 2000 (Soderhall, 1999). The resolution of the whole genome sequence of WSSV facilitates a better understanding on the molecular mechanism underlying the pathogenesis of WSSV in shrimp (Yang et al., 2001). In the last decade, a series of papers around shrimp immunity were published and a batch of related data accumulated, which are very useful for understanding the interaction between shrimp and pathogens to enrich the immune theory of invertebrates. Recently, several review papers summarize the achievements in shrimp immunity including EST sequencing and database construction (Leu et al., 2011), microarray analysis of shrimp immune response (Aoki et al., 2011), shrimp molecular responses to viral pathogen (Flegel and Sritunyalucksana, 2011) and the cationic antimicrobial peptides in penaeid shrimp (Tassanakajon et al., 2010). Obviously understanding the shrimp immunology is necessary to develop an effective strategy for disease control. Two Major State Basic Research Development Programs of China (973 programs) which integrated several research teams from Institute of Oceanology, Chinese Academy of Sciences; Third Institute of Oceanology, State Oceanic Administration; Zhejiang University; SUN YAT-SEN University and Shandong University were performed during 2000–2010 to focus on shrimp immunology and disease control. In this paper we would like to review the progress in shrimp immunology research in mainland of China during the last decade.

2. Screening of immune related genes or proteins by large scale approach

With the rapid development of molecular biology, functional genomics and proteomics developed very quickly and were used to answer questions about the function of DNA and Protein at the levels of genes, RNA transcripts, and protein products. The key characteristics of functional genomics and proteomics studies are their genome-wide or proteome-wide approach to these questions, generally involving high-throughput methods rather than a more traditional "gene-by-gene" approach. Under the situation that the whole genomics of shrimp is not available, functional genomics or proteomics are very powerful to study the immunology of shrimp. Since the beginning of the 21th century, the following approaches, including EST sequencing, cDNA microarray, suppression subtractive hybridization and proteomics have been used to screen immune related genes or proteins on a large scale.

2.1. EST sequencing

ESTs are short cDNA sequences (200–800 nucleotide bases in length) that are generated by single-pass 5′or 3′ end sequencing of clones randomly selected from cDNA libraries. Obtaining expressed sequence tags (ESTs) by partial sequencing of cDNA libraries is an effective means of discovering new genes in organisms with no genomic data available (Adams et al., 1991). To gain more information on the genomics of shrimp, more than 10,000 ESTs have been generated and analyzed from a cephalothorax cDNA library of *F. chinensis*. During the analysis of these ESTs, a total of 3120 unique genes, including 1399 contigs and 1721 singletons, were generated (Xiang et al., 2002, 2008). Among those unique genes, 81 unigenes responding to 428 ESTs were found to have similarity to known immunity-related proteins (Shen et al., 2004). Considering the function of hemocytes in shrimp immunity, the cDNA library of hemocytes was constructed (Zhang et al., 2005). 2371 ESTs were sequenced from cDNA library of hemocytes. Through bio-informatics analysis on these ESTs, 34 genes including 177 ESTs have been annotated to be potentially involved in defense or immune functions in shrimp, based on current knowledge (Dong and Xiang, 2007). The information of aforementioned EST sequences can enrich our understanding on the immune genes of shrimp.

2.2. cDNA microarray

The microarray technique has been proved to be a powerful tool to investigate the expression of thousands of genes in a single